

SEQUENCE LISTING

```
<110> Xiao, Zhi-Cheng
<120> Peptides, Antibodies Thereto, and Their
 Use in the Treatment of Central Nervous System Damage
<130> 0380-P03063US1
<140> US 10/537,648
<141> 2005-06-06
<150> PCT/GB2003/005323
<151> 2003-12-05
<150> US 60/431,620
<151> 2002-12-06
<160> 35
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 7
<212> PRT
<213> Artificial Sequence
<223> From a phage library that displays random 7-mers
<400> 1
Tyr Leu Thr Gln Pro Gln Ser
                 5
1
<210> 2
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> From a phage library that displays random 7-mers
Gly Ser Leu Pro His Ser Leu
<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence
<223> From a phage library that displays random 7-mers
<400> 3
Thr Gln Leu Phe Pro Pro Gln
<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence
<223> From a phage library that displays random 7-mers
```

```
<400> 4
His Ser Ile Pro Asp Asn Ile
<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> From a phage library that displays random 7-mers
<400> 5
His His Met Pro His Asp Lys
<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence
<223> From a phage library that displays random 7-mers
<400> 6
Tyr Thr Thr Pro Pro Ser Pro
<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence
<223> From a phage library that displays random 7-mers
<400> 7
Gln Leu Pro Leu Met Pro Arg
                5
<210> 8
<211> 508
<212> PRT
<213> Rattus norvegicus
<400> 8
Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
                                 10
Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
            20
                                25
                                                    30
Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
                            40
                                                45
Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
    50
                        55
                                            60
Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
                                       75
                                                           80
                    70
Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
                                   90
                85
Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
                                105
                                                   110
            100
Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
                          120
       115
Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
                        135
                                            140
    130
Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
                  150
                                     155
Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
```

```
165
                                 170
His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
                     185
                                                190
         180
Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
                                           2.05
       195
                          200
Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
                                      220
                      215
   210
Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro 225 230 235
                                    235
                 230
225
Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
              245
                                250
Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
                                                270
        260
                           265
Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
                                             285
    275
                          280
Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
                      295
                                         300
Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
                  310
                                     315
Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
                                                   335
              325
                                 330
Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
                              345
                                               350
           340
Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
                                     365
                         360
      355
Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
                                       380
                   375
   370
Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
                390
                                     395
Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
                                                    415
             405
                                410
Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
                             425
                                              430
           420
Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
                         440
                                            445
Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
                      455
                                         460
Arg Ser Gly Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
                470
                                   475
Gln Ala Pro Pro Arg Val Ile Cys Thr Ser Arg Asn Leu Tyr Gly Thr
                            490
          485
Gln Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg
                              505
           500
```

<210> 9 <211> 205 <212> PRT <213> Homo sapiens

Cys Pro Cys Ala Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg Ile Glu Met Leu Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn Ala Asn Cys Cys Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile Pro His Cys Ser Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys Ile Cys Asn Glu Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys Pro Leu Gly Cys Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile Cys Asp Ser Glu Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro Thr Asp Cys Ser Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys Glu Glu Pro Tyr Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly Asp Cys Ser Gly Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu

Glu Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala 165 170 Cys Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu 180 185 Gly Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro 200 <210> 10 <211> 185 <212> PRT <213> Homo sapiens <400> 10 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro 10 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu 20 25 30 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp 35 40 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser 50 55 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp 70 75 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala 95 85 90 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro 105 110 100 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val 125 120 115 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro 140 130 135 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr 155 145 150 Pro Pro Ala Pro Ala Pro Ala Pro Pro Ser Thr Pro Ala Ala Pro 165 170 Lys Arg Arg Gly Ser Ser Gly Ser Val 180 <210> 11 <211> 66 <212> PRT <213> Homo sapiens <400> 11 Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly 10 His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu 25 20 Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr 40 3.5 Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser 50 55 60 Leu Lys 65 <210> 12 <211> 973 <212> PRT <213> Artificial Sequence <220> <223> Fusion protein

<220>

<221> VARIANT <222> (509)...(511) <223> Polyalanine linker

4

```
<220>
<221> VARIANT
<222> (717)...(719)
<223> Polyalanine linker
<220>
<221> VARIANT
<222> (905)...(907)
<223> Polyalanine linker
<400> 12
Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
                                 10
1
Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
           2.0
                               25
Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
                          40
 35
Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
                                          60
                       55
Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
                  70
                                      75
Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
                                  90
               85
Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
                             105
                                               110
          100
Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
                                             125
       115
                           120
Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
                                          140
   130
                       135
Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
                                   155
         150
145
Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
                                                      175
              165
                                   170
His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
                             185
                                                  190
Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
                           200
                                              205
       195
Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
                      215
                                         220
Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro
225
                   230
                                      235
Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
                                                      255
                                  250
               245
Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
                                                 270
                             265
           260
Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
                           280
      275
Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
                      295
                                          300
Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
                   310
                                       315
                                                          320
Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
              325
                                  330
                                                      335
Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
           340
                               345
                                                  350
Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
       355
                           360
                                              365
Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
                                         380
                       375
Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
                                       395
385
                  390
Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
               405
                                 410
Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
                              425
                                                   430
           420
Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
       435
                          440
                                              445
Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
   450
                      455
                                         460
Arg Ser Gly Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
                   470
                                       475
```

```
Gln Ala Pro Pro Arg Val Ile Cys Thr Ser Arg Asn Leu Tyr Gly Thr
                                   490
              485
Gln Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg Ala Ala Cys
           500
                               505
                                                   510
Pro Cys Ala Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg Ile
      515
                           520
                                              525
Glu Met Leu Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn Ala
                       535
                                           540
Asn Cys Cys Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile Pro
                   550
                                      555
His Cys Ser Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys Ile
                                                      575
                                   570
               565
Cys Asn Glu Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys Pro
                               585
                                                  590
           580
Leu Gly Cys Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile Cys
                          600
                                              605
       595
Asp Ser Glu Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro Thr
   610
                       615
                                          620
Asp Cys Ser Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys Glu
                  630
                                      635
625
Glu Pro Tyr Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly Asp
                                   650
             645
Cys Ser Gly Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu Glu
                                                  670
                               665
           660
Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala Cys
                           680
                                               685
Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu Gly
                      695
                                          700
Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro Ala Ala Met
                   710
                                      715
Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro Pro
               725
                                   730
                                                      735
Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu Asp
                                                750
           740
                              745
Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Leu
                                               765
                           760
       755
Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser Ala
                       775
                                           780
Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp Phe
785
                   790
                                      795
Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala Ala
                                  810
                                                      815
               805
Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro Val
                               825
                                                  830
           820
Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val Ser
       835
                           840
                                              845
Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro
   850
                       855
                                          860
Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr Pro
                   870
                                      875
Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys
               885
                                  890
Arg Arg Gly Ser Ser Gly Ser Val Ala Ala Ala Arg Ile Tyr Lys Gly
           900
                               905
Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala
      915
                           920
                                               925
Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr
   930
                       935
                                           940
Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg
                  950
                                      955
Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys
               965
                                   970
```

<210> 13 <211> 1524

<212> DNA

<213> Rattus norvegicus

atgatattcc ttaccaccct gcctctgttt tggataatga tttcagcttc tcgagggggg 60

```
cactggggtg cctggatgcc ctcgtccatc tcagccttcg agggcacgtg tgtctccatc 120
ccctgccgtt tcgacttccc ggatgagctc agaccggctg tggtacatgg cgtctggtat 180
ttcaacagtc cctaccccaa gaactacccg ccagtggtct tcaagtcccg cacacaagtg 240
gtccacgaga gcttccaggg ccgtagccgc ctgttgggag acctgggcct acgaaactgc 300
accetgette teageaeget gagecetgag etgggaggga aataetattt eegaggtgae 360
ctqqqcqqct acaaccagta caccttctcg gagcacagcg tcctggacat catcaacacc 420
cccaacatcg tggtgccccc agaagtggtg gcaggaacgg aagtagaggt cagctgcatg 480
ggggagccca ctgttctggg tcggctgcgg gaggatgaag gcacctgggt gcaggtgtca 600
ctgctacact tcgtgcctac tagagaggcc aacggccacc gtctgggctg tcaggctgcc 660
ttccccaaca ccaccttgca gttcgagggt tacgccagtc tggacgtcaa gtaccccccg 720
gtgattgtgg agatgaattc ctctgtggag gccattgagg gctcccacgt cagcctgctc 780
tgtggggctg acagcaaccc gccaccgctg ctgacttgga tgcgggatgg gatggtgttg 840
agggaggcag ttgctgagag cctgtacctg gatctggagg aggtgacccc agcagaggac 900
ggcatctatg cttgcctggc agagaatgcc tatggccagg acaaccgcac ggtggagctg 960
agcgtcatgt atgcaccttg gaagcccaca gtgaatggga cggtggtggc ggtagagggg 1020
gagacagtct ccatcctgtg ttccacacag agcaacccgg accctattct caccatcttc 1080
aaggagaagc agateetgge caeggteate tatgagagte agetgeaget ggaacteeet 1140
gcagtgacgc ccgaggacga tggggagtac tggtgtgtag ctgagaacca gtatggccag 1200
agagccaccg cettcaacct gtctgtggag tttgctccca taatcettet ggaatcgcae 1260
tgtgcagcgg ccagagacac cgtgcagtgc ctgtgtgtgg taaaatccaa cccggaaccc 1320
tccgtggcct ttgagctgcc ttcccgcaac gtgactgtga acgagacaga gagggagttt 1380
gtgtactcag agcgcagcgg cctcctgctc accagcatcc tcacgctccg gggtcaggcc 1440
caagececae eeegeqteat ttgtacetee aggaacetet aeggeaceca gageetegag 1500
ctgcctttcc agggagcaca ccga
<210> 14
<211> 615
<212> DNA
<213> Homo sapiens
<400> 14
tgtccatgtg ccagttcagc ccaggtgctg caggagctgc tgagccggat cgagatgctg 60
gagagggagg tgtcggtgct gcgagaccag tgcaacgcca actgctgcca agaaagtgct 120
gccacaggac aactggacta tatccctcac tgcagtggcc acggcaactt tagctttgag 180
tcctgtggct gcatctgcaa cgaaggctgg tttggcaaga attgctcgga gccctactgc 240
ccgctgggtt gctccagccg gggggtgtgt gtggatggcc agtgcatctg tgacagcgaa 300
tacagegggg atgactgttc egaacteegg tgeccaacag actgeagete eegggggete 360
tgcgtggacg gggagtgtgt ctgtgaagag ccctacactg gcgaggactg cagggaactg 420
aggtgccctg gggactgttc ggggaagggg agatgtgcca acggtacctg tttatgcgag 480
gagggctacg ttggtgagga ctgcggccag cggcagtgtc tgaatgcctg cagtgggcga 540
ggacaatgtg aggagggct ctgcgtctgt gaagagggct accagggccc tgactgctca 600
gcagttgccc ctcca
<210> 15
<211> 555
<212> DNA
<213> Homo sapiens
<400> 15
atggaagacc tggaccagtc tcctctggtc tcgtcctcgg acagcccacc ccggccgcag 60
cccgcgttca agtaccagtt cgtgagggag cccgaggacg aggaggaaga agaggaggag 120
gaagaggagg acgaggacga agacctggag gagctggagg tgctggagag gaagcccgcc 180
gccgggctgt ccgcggccc agtgcccacc gccctgccg ccggcgccc cctgatggac 240 ttcggaaatg acttcgtgcc gccggcgcc cggggacccc tgccggcgc tcccccgtc 300
gcccggagc ggcagccgtc ttgggacccg agcccggtgt cgtcgaccgt gcccgcgcca 360
teccegetgt etgetgeege agtetegeee tecaagetee etgaggaega egageeteeg 420
gcccggcctc ccctcctcc cccggccagc gtgagccccc aggcagagcc cgtgtggacc 480
ccgccagccc cggctcccgc cgcgcccccc tccaccccgg ccgcgcccaa gcgcaggggc 540
tcctcgggct cagtg
<210> 16
<211> 198
<212> DNA
<213> Homo sapiens
<400> 16
aggatataca agggtgtgat ccaagctatc cagaaatcag atgaaggcca cccattcagg 60
gcatatctgg aatctgaagt tgctatatct gaggagttgg ttcagaagta cagtaattct 120
gctcttggtc atgtgaactg cacgataaag gaactcaggc gcctcttctt agttgatgat 180
ttagttgatt ctctgaag
```

<210> 17 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> PCR primer MAG1	
<400> 17 cgggatccat gatattcctt accaccct	28
<210> 18 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> PCR primer MAG2	
<400> 18 tccccgcggc tcggtgtgct ccctggaa	28
<210> 19 <211> 29 <212> DNA <213> Artificial Sequence	
<220> <223> PCR primer TNR1	
<400> 19 tccccgcggc atgtccatgt gccagttca	29
<pre> '<210> 20 <211> 28 <212> DNA <213> Artificial Sequence</pre>	
<220> <223> PCR primer TNR2	
<400> 20 ttgcggccgc tggaggggca actgctga	28
<210> 21 <211> 32 <212> DNA <213> Artificial Sequence	
<220> <223> PCR primer NogoN1	
<400> 21 ttgcggccgc aatggaagac ctggaccagt ct	32
<210> 22 <211> 31 <212> DNA <213> Artificial Sequence	
<220> <223> PCR primer NogoN2	
<400> 22 aaactgcagc cactgagccc gaggagcccc t	31
<210> 23 <211> 28 <212> DNA <213> Artificial Sequence	

```
<220>
<223> PCR primer Nogo66-1
<400> 23
aaactgcagc aaggatatac aagggtgt
                                                                 2.8
<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer Nogo66-2
<400> 24
                                                                 28
gctctagatc acttcagaga atcaacta
<210> 25
<211> 2934
<212> DNA
<213> Artificial Sequence
<220>
<223> Construct resulting from sequentially connected
     PCR products
<400> 25
ggatccatga tattccttac caccctgcct ctgttttgga taatgatttc agcttctcga 60
ggggggcact ggggtgcctg gatgccctcg tccatctcag ccttcgaggg cacgtgtgtc 120
tccatcccct gccgtttcga cttcccggat gagctcagac cggctgtggt acatggcgtc 180
tggtatttca acagtcccta ccccaagaac tacccgccag tggtcttcaa gtcccgcaca 240
caagtggtcc acgagagctt ccagggccgt agccgcctgt tgggagacct gggcctacga 300
aactgcaccc tgcttctcag cacgctgagc cctgagctgg gagggaaata ctatttccga 360
qqtqacctqq qcggctacaa ccagtacacc ttctcggagc acagcgtcct ggacatcatc 420
aacaccccca acatcgtggt gcccccagaa gtggtggcag gaacggaagt agaggtcagc 480
tgcatggtgc cggacaactg cccagagctg cgccctgagc tgagctggct gggccacgag 540
gggctagggg agcccactgt tctgggtcgg ctgcgggagg atgaaggcac ctgggtgcag 600
gtgtcactgc tacacttcgt gcctactaga gaggccaacg gccaccgtct gggctgtcag 660
gctgccttcc ccaacaccac cttgcagttc gagggttacg ccagtctgga cgtcaagtac
ccccggtga ttgtggagat gaattcctct gtggaggcca ttgagggctc ccacgtcagc 780
gtgttgaggg aggcagttgc tgagagcctg tacctggatc tggaggaggt gaccccagca 900
qaqqacggca tetatgettg cetggcagag aatgeetatg gecaggacaa eegcacggtg 960
gagctgagcg tcatgtatgc accttggaag cccacagtga atgggacggt ggtggcggta 1020
gaggggaga cagtetecat cetgtgttee acacagagea acceggacee tatteteace 1080
atcttcaagg agaagcagat cctggccacg gtcatctatg agagtcagct gcagctggaa 1140
ctccctgcag tgacgcccga ggacgatggg gagtactggt gtgtagctga gaaccagtat 1200
ggccagagag ccaccgcctt caacctgtct gtggagtttg ctcccataat ccttctggaa 1260
tegeaetgtg cageggeeag agacaeegtg cagtgeetgt gtgtggtaaa ateeaaeeeg 1320
gaaccttcg tggcctttga gctgccttcc cgcaacgtga ctgtgaacga gacagagagg 1380
gagtttgtgt actcagagcg cagcggcctc ctgctcacca gcatcctcac gctccggggt 1440
caqqcccaag ccccacccg cgtcatttgt acctccagga acctctacgg cacccagagc 1500
ctcgagctgc ctttccaggg agcacaccga gccgcggcat gtccatgtgc cagttcagcc 1560
caggtgctgc aggagctgct gagccggatc gagatgctgg agagggaggt gtcggtgctg 1620
cgagaccagt gcaacgccaa ctgctgccaa gaaagtgctg ccacaggaca actggactat 1680
atccctcact gcagtggcca cggcaacttt agcttttgagt cctgtggctg catctgcaac 1740
qaaqqctqqt ttqqcaaqaa ttqctcqqaq ccctactqcc cqctqqqttq ctccaqccqq 1800
ggggtgtgtg tggatggcca gtgcatctgt gacagcgaat acagcgggga tgactgttcc 1860
gaactccggt gcccaacaga ctgcagctcc cgggggctct gcgtggacgg ggagtgtgtc 1920
tgtgaagagc cctacactgg cgaggactgc agggaactga ggtgccctgg ggactgttcg 1980
gggaagggga gatgtgccaa cggtacctgt ttatgcgagg agggctacgt tggtgaggac 2040
tgcqqccaqc ggcagtgtct gaatgcctgc agtgggcgag gacaatgtga ggaggggctc 2100
tgcgtctgtg aagagggcta ccagggccct gactgctcag cagttgcccc tccagcggcc 2160
gcaatggaag acctggacca gtctcctctg gtctcgtcct cggacagccc accccggccg 2220
cagcccgcgt tcaagtacca gttcgtgagg gagcccgagg acgaggagga agaagaggag 2280
gaggaagagg aggacgagga cgaagacctg gaggagctgg aggtgctgga gaggaagccc 2340
qccqccqggc tgtccgcggc cccagtgccc accgcccttg ccgccggcgc gcccctgatg 2400
gactteggaa atgacttegt geegeeggeg eeceggggae eeetgeegge egeteeeee 2460
gtcgccccgg agcggcagcc gtcttgggac ccgagcccgg tgtcgtcgac cgtgcccgcg 2520
ccatccccgc tgtctgctgc cgcagtctcg ccctccaagc tccctgagga cgacgagcct 2580
```

```
coggeocogge etececetee tececoggee agegtgagee eccaggeaga geocgtgtgg 2640
accocgocag coccggetec cgccgcgccc ccctccaccc cggccgcgcc caagcgcagg 2700
ggctcctcgg gctcagtggc tgcagcaagg atatacaagg gtgtgatcca agctatccag 2760
aaatcagatg aaggccaccc attcagggca tatctggaat ctgaagttgc tatatctgag 2820
gagttggttc agaagtacag taattctgct cttggtcatg tgaactgcac gataaaggaa 2880
ctcaggcgcc tcttcttagt tgatgattta gttgattctc tgaagtgatc taga
<210> 26
<211> 42
<212> DNA
<213> M13 coliphage
<400> 26
ttattcgcaa ttcctttagt ggtacctttc tattctcact ct
                                                                    42
<210> 27
<211> 33
<212> DNA
<213> M13 coliphage
<400> 27
ggtggaggtt cggccgaaac tgttgaaagt tgt
                                                                    33
<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Exemplary 7-mer peptide-encoding sequence
<400> 28
                                                                    21
tatctgacgc agcctcagtc g
<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Exemplary 7-mer peptide-encoding sequence
<400> 29
                                                                    21
ggttctctgc ctcattcgct g
<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence
<223> Exemplary 7-mer peptide-encoding sequence
<400> 30
                                                                    21
acgcagctgt ttcctcctta g
<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Exemplary 7-mer peptide-encoding sequence
<400> 31
cattctattc ctgataatat t
                                                                   21
<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence
```

<pre><223> Exemplary 7-mer peptide-encoding sequence</pre>	
<400> 32	21
catcatatgc ctcatgataa g	21
<210> 33	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
.000	
<pre><220> <223> Exemplary 7-mer peptide-encoding sequence</pre>	
(223) Exemplary /-mer peptide-encoding sequence	
<400> 33	
tatacgacgc ctccgagtcc t	21
<210> 34	
<211> 21 <212> DNA	
<213> Artificial Sequence	
1220 Marian	
<220>	
<223> Exemplary 7-mer peptide-encoding sequence	
.400. 24	
<400> 34 cagetteege ttatgeeteg t	21
cagetteege ttatgeeteg t	
<210> 35	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<pre><223> Exemplary 7-mer peptide-encoding sequence</pre>	
<400> 35	
acgcagctgt ttcctcctca g	21